Remarks

Reconsideration of this Application is respectfully requested.

Upon entry of the foregoing amendments, claims 95-147 are active in the application, with claims 95, 98, 101, 104, 115, 117, 127, and 136 being the independent claims. The amendments are being made to place the case in condition for allowance, especially after the helpful Examiner interview on September 12, 2001, or in better form for consideration on appeal. Support for the amendments to claims 95, 98, and 115 can be found at, *inter alia*, pages 94-101 (Example 6). Accordingly, the amendments are believed to introduce no new matter, and their entry is respectfully requested.

Based on the above amendments and the following remarks, Applicants respectfully request that the Examiner reconsider all outstanding objections and rejections and that they be withdrawn.

Examiner Interview

Applicants gratefully acknowledge the courtesy extended by Examiners Landsman and Romeo to the undersigned, in-house counsel for the assignee, and a technical specialist employed by the assignee, in a personal interview held on September 12, 2001. The Examiner Interview Summary Record prepared by Examiner Landsman accurately reflects the substance of the interview.

Rejection Under 35 U.S.C. § 101

The Examiner has maintained the rejection under 35 U.S.C. § 101 for the reasons of record stated on pages 4-5 of the Office Action dated December 20, 2000. Briefly, the Examiner contends that the claimed invention is not supported by a specific, substantial, and credible asserted utility or well-established utility. Applicants respectfully traverse this rejection.

In their Response filed March 20, 2001, Applicants, *inter alia*, argued that Example 6 of the specification (pages 94-96) disclosed that the transfection of the epsilon subunit into cells produced GABA-activated currents (Figure 5) and binding sites (Figure 6). However, as stated by the Examiner at page 3 of Paper No. 20, and discussed at the personal interview on September 12, 2001, it was not clear to the Examiner that the polynucleotide of SEQ ID NO:41 (or more particularly, the polypeptide of SEQ ID NO:42) was responsible for the results reported in Figures 5 and 6. During the September 12 , 2001 personal interview, Applicants and their representatives clarified that the claimed protein, as represented by SEQ ID NO:42, was responsible for the effects shown in Figures 5 and 6. The Examiner acknowledged that this issue was resolved, since Applicants have provided a specific, substantial, and credible utility. Reconsideration and withdrawal of this rejection under 35 U.S.C. § 101 is respectfully requested.

Rejections Under 35 U.S.C. § 112, First Paragraph

A. The Examiner maintained the rejection under 35 U.S.C. § 112, first paragraph,

for lack of enablement grounded on the alleged lack of utility (*i.e.*, the "how to use" aspect of 112, first paragraph, has not been satisfied).

Since the utility rejection has been overcome (see above), Applicants believe that this aspect of the 112, first rejection, has been overcome as well. Reconsideration and withdrawal of this rejection are respectfully requested.

B. The Examiner also maintained the rejection of claims 95, 98, 101, 104, 107-117 and 119-147 for reasons set forth at pages 6-7 of the Office Action dated December 20, 2000. Briefly, the Examiner contends that the specification does not reasonably provide enablement for polypeptides which are "at least 95% identical" to various amino acid segments of SEQ ID NO:42, and does not enable a person skilled in the art to make and/or use the invention commensurate in scope with the claims. Applicants respectfully traverse this rejection.

Solely to expedite allowance and without acquiescing to the propriety of the rejection, and based on the helpful discussion with the Examiner on September 12, 2001, Applicants have amended the claims to recite that the polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits. Applicants believe that this rejection is now moot. Reconsideration and withdrawal of this rejection are respectfully requested.

Conclusion

All of the stated grounds of rejection have been properly traversed, accommodated, or rendered moot. Applicants therefore respectfully request that the Examiner reconsider

all presently outstanding objections and rejections and that they be withdrawn. Applicants believe that a full and complete reply has been made to the outstanding Office Action and, as such, the present application is in condition for allowance. If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Prompt and favorable consideration of this Amendment and Reply is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

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Version with markings to show changes made

95. (thrice amended) An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 260 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

98. (thrice amended) An [The] isolated polynucleotide [of claim 95, wherein said] comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence [is] at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids 1 to 488 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

101. (thrice amended) An [The] isolated polynucleotide [of claim 98, wherein said] comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence [is] at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids -17 to 488 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

104. (thrice amended) An [The] isolated polynucleotide [of claim 101, wherein said] comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence [is] at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42;

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of residues in amino acids -18 to 488 of SEQ ID NO:42; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

115. (thrice amended) An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,

wherein % identity is determined with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

117. (thrice amended) [The] An isolated polynucleotide [of claim 115, wherein said] encoding a polypeptide comprising an amino acid sequence [is] at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;

wherein % identity is determined with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642; and

wherein said polypeptide forms a $GABA_A$ receptor complex with α- and β- $GABA_A$ receptor subunits.

118. (once amended) The isolated polynucleotide of claim 117, wherein the polypeptide comprises [comprising] the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.